Validation of consistency of Mendelian sampling variance in national evaluation models

A.-M. Tyrisevä[1], E. A. Mäntysaari[1], J. Jakobsen[2], G. P. Aamand[3], J. Dürr[2], W. F. Fikse[4], M. H. Lidauer[1]

[1]*MTT Agrifood Research Finland, Biotechnology and Food Research, Biometrical Genetics, Jokioinen, Finland*
[2]*Interbull Centre, Department of Animal Breeding and Genetics, SLU, Uppsala, Sweden*
[3]*NAV Nordic Cattle Genetic Evaluation, Aarhus, Denmark*
[4]*Dept. Animal Breeding and Genetics, SLU, Uppsala, Sweden*

Introduction

Trends in genetic variance benefit bulls coming from populations or year classes with increased genetic variance and lead to sub-optimal selection decisions. Therefore, national evaluation centers and Interbull need a method to observe possible trends in genetic variance.

Two different methods to estimate within-year genetic variance have been published (Fikse et al. 2003, Lidauer et al. 2007). Fikse et al. continued their work by presenting a procedure to obtain tolerance intervals for the within-year genetic variances (Fikse et al. 2005). It was tested using field data sets, but has not been implemented yet. The aim of this research project was to further dissect the behavior of both methods by performing a simulation study (Tyrisevä et al. 2011) and to develop a test to validate the consistency of Mendelian sampling variance in national evaluation models, which is outlined in this paper.

Validation procedure

Data edits

The test can be performed either for cows or bulls. A time period of 12 most recent birth year classes is covered. In the most recent birth year class of that period, the number of animals with observations should be at least 50% of the average yearly size of the animals in the testing period. EBVs for animals and their parents are needed, as well as the estimates of reliability. Since EBVs are used to calculate the Mendelian sampling terms only animals with both parents identified are used.

Estimation of genetic variance

Within-year genetic variance is estimated according to Fikse et al. (2005). We use the accelerated version (IB4) that implicitly expresses the prediction error variance on a relative scale, in unit genetic variance, and as such is only influenced by the heritability of the trait. Thus, it does not need to assume a particular value for the genetic variance:

$$\sigma^2_{u_i} = \frac{\sum_{k=1}^{q_i} d_k \hat{m}_k^2}{q_i - \sum_{k=1}^{q_i} d_k PEV(\hat{m}_k)}, \qquad (1)$$

where q_i is the number of animals in year i, d_k is the inverse of the proportion of the genetic variance not explained by the known parents, $\hat{m}_k^2$ is the squared estimated Mendelian sampling deviation of animal k. $PEV(\hat{m}_k)$ is the prediction error variance of the Mendelian sampling deviation that is approximated according to Fikse et al. (2003).

Statistical test

A possible trend is tested for by fitting a weighted regression model for estimates of within-year genetic variances y_i with number of animals used as weights:

$$y_i = b0 + b1 * year_i + e_i \qquad (2)$$

Based on the earlier field test results, only a linear term is needed, when testing is performed on a short time period. An empirical 95% confidence interval for a trend is calculated by bootstrapping data with 1000 case resampling within year classes. For each bootstrapped sample a weighted regression model is fitted and *b0* and *b1* and residual terms are saved. The empirical CI is calculated for a trend that is expressed as a percentage change in genetic variance (*b1*/*b0**100%).

Possible outliers that do not fit the model are identified by calculating residuals from the model (2) within each bootstrap sample. From the samples, 0.025 and 0.975 quantiles are used to determine the 95% confidence intervals for the residuals. If the confidence interval does not include 0.0, then variance estimate of that year is considered as an outlier.

Tolerated level of bias

For large populations such as Holstein cows, the test has a power to detect very small deviations from zero trend that have no practical impact. Thus, there must be pre-specified level of acceptable bias that any population can have.

Validation of the validation procedure

Application

Test data sets were constructed by replacing test-day observations of about 800 000 Danish Holstein cows from 2000 herds with simulated observations based on different variance scenarios. Two scenarios were simulated: Scenario A with a homogenous variance served as a control and for Scenario B, a yearly trend of 2% in phenotypic variance was generated. Breeding values were predicted with the Nordic test-day model. An adjustment for heterogeneous residual variance (HV) was either carried out or not (noHV). Estimates for the additive genetic effects of the random regression coefficients were combined to 305-d EBVs. Cows (I) and bulls (II) were investigated. We also picked up a subsample of the above data to mimic small bull populations (III) such as Nordic Jerseys.

Average number of the animals in year classes was 45 000, 300 and 27 for cows (I), all bulls (II), and bulls in data subset (III), respectively. Details of the data sets and simulations are shown in Tyrisevä et al. (2011). For each of the three test populations, 20 replicates were analyzed. Full model sampling (FMS) served as a control and was used to estimate genetic variance (Lidauer et al. 2007, Tyrisevä et al. 2011). For bulls, five FMS samples were employed to decrease the Monte Carlo noise.

Effect of bias

To qualify the effect of biased mean or biased variance on true EBVs and indices, a simulation study was carried out. True breeding values with a yearly increase of two units and SD of 11 units were generated for 5000 bulls in 10 year classes. Bulls differed between classes and were not related. Each bull had 50 daughters and reliability of 0.83, h^2 was 0.35. For each bull, indices were calculated under different levels of bias (see Figures 4 and 5) and bulls were sorted a) based on their true EBVs or b) based on their indices. Best 1% of the bulls were selected and the means of their EBVs and indices were studied.

Results and Discussion

Estimation of genetic variance

Estimated within-year genetic variances obtained under IB4 and FMS were very similar for bulls (Figure 1). For cows, estimates from IB4 were on a higher level compared to those from FMS (Figure 2), with notable differences in the estimates of first and last year classes. Major part of the cows in these classes had reliability values below 0.50. By removing all the cows with reliability values lower than 0.50, both peaks disappeared and overall level of genetic variance was closer to that obtained under FMS. Fikse et al. (2003) have also noticed that the quality of estimation of genetic variance was associated with the level of PEV that was further affected by the level of approximated reliabilities. Since the data cannot be restricted by the level of reliability values without causing a possible selection bias, it should be restricted by using a time period that ensures use of data with good quality.

A slight decreasing trend observed in the within-year genetic variances in Scenario A in the previous paper (Tyrisevä et al. 2011) was found to be due to inbreeding that was not accounted for. For both cows and bulls, the coefficient of inbreeding was around 1% in the first years and increased to 4.5% in the later years, causing a negative trend of 3% in genetic variance. By modeling inbreeding in the prediction of breeding values and in the estimation of genetic variances, the decreasing trend disappeared. On the other hand, if the inbreeding was accounted for only in the prediction of the breeding values or only in the estimation of genetic variances, bias was higher compared to the situation, when inbreeding was not accounted for at all.

Sample size

Populations such as I and II were found to be of sufficient size to be used in the testing. On the other hand, the estimates of genetic variance in population III were associated with a large sampling error (Figure 3) and application of the validation procedure to so small populations might be difficult.

Test

For both populations I and II, a generated trend in variance, which was not accounted for in the evaluations, was detected by the test in all cases (Tables 1 and 3). Applying heterogeneous variance adjustment resulted in a slight decreasing trend in the genetic variance (Tables 2 and 4). This implies that the HV adjustment over-corrected the bias. The negative bias was on average -0.16%, and it was found as a statistically significant deviation from zero in all the cow data replicates with large year classes. In bulls, only one replicate out of 20 was significantly different from zero. These results illustrate a need to define a level of bias that has no practical meaning for selection decisions and can thus be tolerated.

Outliers were tested for small bull data sets to illustrate the method (Figure 3). Results indicated that the method is able to detect observations that do not fit the model.

Tolerated bias

Top 1% of the bulls represented mainly three newest year classes in all studied bias classes. The two youngest year classes were over-represented by 1 to 3%, when a bias of 2% was introduced. A bias of 2% in the mean and in the variance both resulted in an upward bias of almost 0.2 genetic standard deviations in the group of top 1% bulls, but practically in no loss in the mean of true EBVs of selected animals. Results were supported by those obtained in a simulation study by Fikse (pers. comm.).

The ranking of 10 best bulls were also compared in Scenario A and in B without HV adjustment (Table 5). On average, 86% of the bulls remained in top 10 group in Scenario B.

Provided the tolerated bias was set to 2%, all data replicates in Table 4 would have passed the test, as well as the one failed replicate in Table 2, whereas only those exceeding the level of 2% would have failed in Tables 1 and 3.

Conclusions

A proposed procedure to validate consistency of Mendelian sampling variance in national evaluation models consists of the following steps: estimating within-year genetic variances, fitting a weighted regression model on them, identifying possible outliers that do not fit the model and defining 95% empirical CI for a trend. The tested population fails the test, if its trend deviates significantly from zero and the trend exceeds the tolerated level of bias.

Estimates of within-year genetic variances from IB4 and FMS were in a good agreement for bulls. For cows, IB4 was less robust for low reliability values than FMS and data used for testing should be carefully defined. Use of populations with the yearly sample size as small as in population III should be avoided. Results of this study indicate that a tolerated bias of 2% might be suitable.

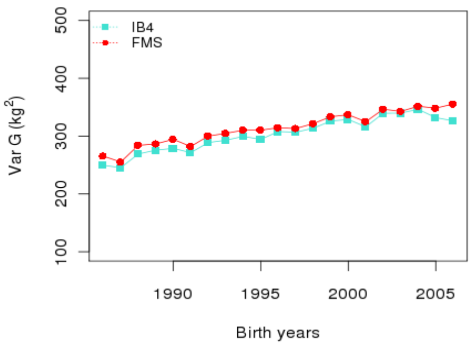

Figure 1. Within-year genetic variances under FMS and IB4 methods for bulls. Estimates are averaged over 20 replicates. Scenario B without adjustment for heterogeneity.

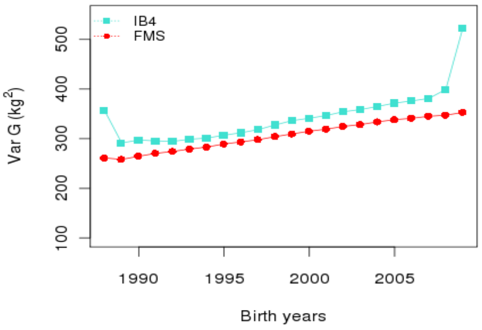

Figure 2. Within-year genetic variances under FMS and IB4 methods for cows. Estimates are averaged over 20 replicates. Scenario B without adjustment for heterogeneity.

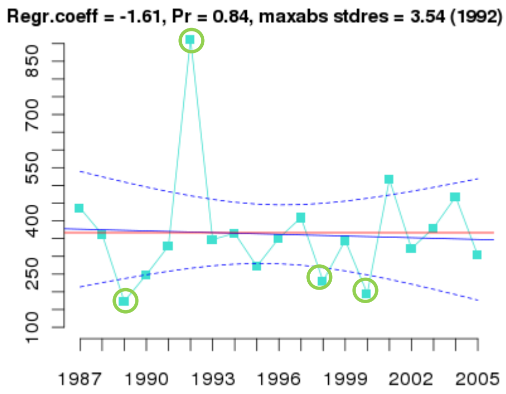

Figure 3. Estimates of within year genetic variances in turquoise for a small bull data set under Scenario B without HV correction. Overall mean of the genetic variance in red. Regression curve and its CI in blue. Detected outliers marked with green circles.

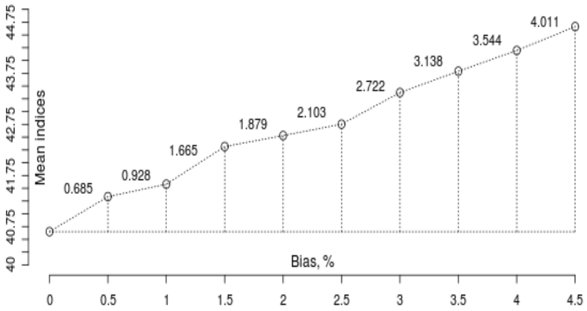

Figure 4. Effect of bias in mean on indices among top 1% of bulls selected from the population spanning 10 years.

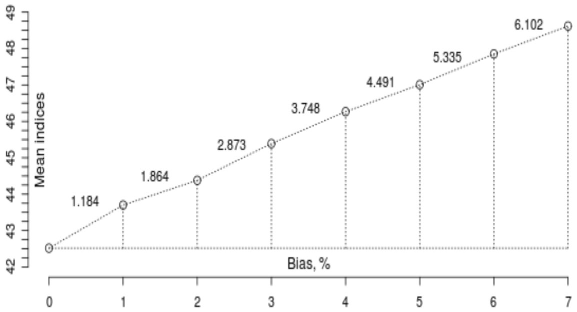

Figure 5. Effect of bias in variance on indices among top 1% of bulls selected from the population spanning 10 years.

Table 1. Empirical CIs for 20 bull data replicates under Scenario B without HV correction. B0 and B1 are means of 1000 bootstrapped samples.

B0	B1	LCI[a]	Trend[b]	UCI[a]	SS[c]
260,0	4,61	0,67	1,81	3,13	s
237,2	5,28	1,07	2,27	3,73	s
254,6	3,87	0,51	1,56	2,83	s
255,1	4,74	0,65	1,91	3,37	s
256,4	4,25	0,59	1,70	3,00	s
254,8	4,04	0,61	1,62	2,70	s
262,7	3,22	0,21	1,26	2,53	s
270,5	3,49	0,34	1,32	2,47	s
244,6	4,56	0,76	1,90	3,28	s
226,2	6,19	1,42	2,80	4,63	s
263,9	4,61	0,63	1,79	3,15	s
221,8	6,10	1,48	2,81	4,57	s
263,6	3,68	0,33	1,44	2,70	s
264,4	3,74	0,28	1,46	2,83	s
265,8	2,78	0,03	1,08	2,24	s
249,2	4,65	0,80	1,91	3,21	s
221,1	6,45	1,50	2,98	4,74	s
275,1	3,09	0,16	1,16	2,34	s
236,8	6,47	1,45	2,79	4,51	s
252,7	4,17	0,62	1,68	2,92	s

[a] Lower and upper confidence intervals

[b] (B1/B0)*100, CIs expressed on a same scale

[c] S refers to statistically significant deviation from zero, ns to statistically non-significant deviation

Table 2. Empirical CIs for 20 bull data replicates under Scenario B with HV correction.

B0	B1	LCI	Trend	UCI	SS
363,5	-0,97	-0,96	-0,25	0,55	ns
335,3	-0,02	-0,70	0,02	0,84	ns
353,8	-1,43	-1,04	-0,39	0,38	ns
359,5	-0,87	-1,00	-0,22	0,63	ns
353,2	-0,90	-0,92	-0,24	0,53	ns
353,4	-1,22	-0,95	-0,33	0,34	ns
363,6	-2,21	-1,24	-0,59	0,13	ns
370,1	-1,80	-1,10	-0,47	0,25	ns
343,5	-0,72	-0,89	-0,19	0,63	ns
323,7	1,00	-0,49	0,34	1,34	ns
371,0	-1,15	-1,00	-0,29	0,47	ns
314,8	1,14	-0,41	0,39	1,34	ns
363,2	-1,63	-1,12	-0,43	0,33	ns
363,5	-1,54	-1,13	-0,40	0,43	ns
369,1	-2,82	-1,39	-0,75	-0,06	s
346,9	-0,59	-0,85	-0,15	0,63	ns
314,3	1,49	-0,36	0,50	1,47	ns
381,0	-2,61	-1,28	-0,67	0,05	ns
339,6	0,91	-0,50	0,29	1,25	ns
340,4	1,06	-0,45	0,34	1,30	ns

Table 3. Empirical CIs for 20 cow data replicates under Scenario B without HV correction.

B0	B1	LCI	Trend	UCI	SS
245,1	4,86	1,88	1,98	2,09	s
243,5	5,08	1,98	2,09	2,19	s
245,2	4,91	1,89	2,00	2,11	s
245,4	4,89	1,89	1,99	2,11	s
242,0	5,11	1,99	2,11	2,23	s
246,1	4,75	1,82	1,93	2,03	s
246,7	4,76	1,82	1,93	2,04	s
242,3	5,16	2,02	2,13	2,24	s
242,3	5,11	2,00	2,11	2,22	s
241,8	5,14	2,02	2,13	2,24	s
246,7	4,80	1,84	1,95	2,05	s
245,5	4,80	1,84	1,96	2,07	s
249,6	4,54	1,71	1,82	1,93	s
243,6	4,97	1,92	2,04	2,16	s
246,5	4,75	1,82	1,93	2,04	s
244,2	4,96	1,92	2,03	2,14	s
246,4	4,75	1,82	1,93	2,05	s
245,8	4,85	1,86	1,97	2,08	s
245,8	4,87	1,87	1,98	2,08	s
243,0	5,06	1,97	2,08	2,20	s

Table 4. Empirical CIs for 20 cow data replicates under Scenario B with HV correction.

B0	B1	LCI	Trend	UCI	SS
339,2	-0,62	-0,25	-0,18	-0,11	s
337,4	-0,38	-0,18	-0,11	-0,04	s
338,2	-0,47	-0,21	-0,14	-0,07	s
339,2	-0,57	-0,24	-0,17	-0,09	s
335,3	-0,31	-0,17	-0,09	-0,02	s
339,9	-0,70	-0,27	-0,21	-0,14	s
340,5	-0,70	-0,28	-0,20	-0,13	s
336,0	-0,29	-0,15	-0,09	-0,02	s
335,8	-0,32	-0,17	-0,10	-0,02	s
335,0	-0,28	-0,15	-0,08	-0,01	s
341,0	-0,69	-0,26	-0,20	-0,14	s
339,1	-0,62	-0,26	-0,18	-0,11	s
344,0	-0,93	-0,34	-0,27	-0,20	s
337,4	-0,46	-0,21	-0,14	-0,06	s
340,2	-0,72	-0,28	-0,21	-0,14	s
338,0	-0,49	-0,22	-0,14	-0,08	s
340,1	-0,68	-0,27	-0,20	-0,12	s
340,5	-0,68	-0,27	-0,20	-0,13	s
339,6	-0,57	-0,24	-0,17	-0,10	s
338,5	-0,50	-0,22	-0,15	-0,07	s

Table 5. Effect of the yearly bias of 2% in genetic variance on top 10 bull rankings.

A scen, TOP 10	Ranking of the TOP 10 bulls in B scen, when no HV adjustment																			
	Data replicates																			
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	2	3	1	1	2	1
2	2	2	2	3	2	4	2	2	2	4	2	2	2	2	1	5	2	2	1	2
3	4	3	5	2	3	2	5	3	3	1	3	4	3	3	3	1	4	3	5	3
4	3	4	3	8	4	3	3	4	8	2	4	3	5	4	6	4	3	9	9	4
5	12	6	7	4	7	5	4	7	5	6	13	5	4	5	5	7	5	4	3	5
6	8	8	10	5	5	10	6	8	7	5	7	6	6	8	8	2	6	5	4	6
7	7	11	4	6	6	7	10	5	4	7	15	9	16	7	4	6	9	6	8	7
8	5	7	12	11	9	6	13	10	6	9	11	7	10	6	9	8	7	12	7	8
9	13	9	6	7	8	8	8	11	11	8	8	13	7	13	12	18	13	7	6	11
10	6	5	13	9	12	9	7	6	13	14	17	12	9	9	7	12	12	8	13	22
Pr[a]	80	90	80	90	90	100	90	90	80	90	60	80	90	90	90	80	80	90	90	80

[a] Proportion of bulls that remained among top 10 bulls

Acknowledgements

The project work has been jointly funded by MTT, NAV and Interbull. The data for the analyses has been received from NAV.

References

Fikse, W.F., Klei, L., Liu, Z. and Sullivan, P.G. 2003. Procedure for validation of trends in genetic variance. Interbull Bull, 31:30–36.

Fikse, W.F., Liu, Z. and Sullivan, P.G. 2005. Tolerance values for validation of trends in genetic variances over time. Interbull Bull, 33: 200-203.

Lidauer, M., Vuori, K., Strandén, I. and Mäntysaari, E.A. 2007. Experiences with Interbull test iv: estimation of genetic variance. Interbull Bull, 37:69–72.

Tyrisevä, A.-M., Mäntysaari, E.A., Fikse, F. and Lidauer, M.H. 2011. Simulation study on Mendelian sampling variance tests. Interbull Bull, 44: 57-61.